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Oxygen isotope composition of sulfate produced during microbial sulfur oxidation: A pathway-specific fingerprint?

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The oxidation of zero-valent sulfur such as elemental sulfur (S0) is an important energy source in many marine habitats including deep-sea vents, pelagic redox-clines and coastal surface sediments. Many microorganisms oxidize elemental sulfur to sulfate to gain reducing power. This transformation is catalyzed by a few known enzymatic pathways such as the reverse dissimilatory sulfite reductase (rDSR)-aprAB/Sor pathway or the Sox multienzyme pathway. The isotopic composition of oxygen and sulfur in produced sulfate (δ34S and δ18O) is determined by the isotope composition of the reactants, the ratio between forward and backward fluxes of enzymatically catalyzed reaction steps, and by kinetic and equilibrium isotopic fractionation. We hypothesize that the activity of distinct oxidation pathways is reflected in different δ34S and particularly, in unique δ18O isotopic fingerprints in the produced sulfate.
To test our hypothesis we grew pure cultures of photo- and chemoautotrophic sulfur-oxidizing microorganisms of different phylogenetic origin with S0 as sole source of reducing power and determined the sulfur and oxygen isotope composition of the produced sulfate. The identification of characteristic isotope fingerprints for each sulfur oxidation pathway could serve as a tool to estimate and deduce the importance of certain enzymatic pathways and sulfur-oxidizing microorganisms in the environment.